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Chromatin dynamics during interphase and cell division: similarities and differences between model and crop plants

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Abstract

Genetic information in the cell nucleus controls organismal development, responses to the environment and finally ensures own transmission to the next generations. To achieve so many different tasks, the genetic information is associated with structural and regulatory proteins, which orchestrate nuclear functions in time and space. Furthermore, plant life strategies require chromatin plasticity to allow a rapid adaptation to abiotic and biotic stresses. Here, we summarize current knowledge on the organisation of plant chromatin and dynamics of chromosomes during interphase and mitotic and meiotic cell divisions for model and crop plants differing as to the genome size, ploidy and amount of genomic resources available. The existing data indicate that chromatin changes accompany most (if not all) cellular processes and that there are both shared and unique themes in the chromatin structure and global chromosome dynamics among species. Ongoing efforts to understand the molecular mechanisms involved in chromatin organisation and remodeling have, together with the latest genome editing tools, potential to unlock crop genomes for innovative breeding strategies and improvements of various traits.

Keywords: Chromatin, epigenetics, chromosome, mitosis, meiosis, plant development, plant breeding, crops, Arabidopsis.

Introduction

Most eukaryotic DNA, the carrier of genetic information, is stored in cell nuclei as linear supermolecules - the chromosomes. Complexes of nuclear DNA with the associated proteins constitute chromatin, which is required for proper DNA packaging, regulation of gene expression and chromosome organisation. The basic units of chromatin are the nucleosomes, which consist of approximately 146 bp of DNA wrapped around a histone octamer having two copies of each of the H2A, H2B, H3 and H4 (reviewed in e.g. McGinty and Tan, 2015).

Replacing the canonical histones with non-canonical ones leads to different chromatin functions (Koyama and Kurumizaka, 2018). Data from the model species *Arabidopsis thaliana* (Arabidopsis) suggest functional diversification of histone H1, H2A and H3 proteins. Histones H1.1 and H1.2 represent the canonical forms, but H1.3 is a stress inducible variant (Rutowicz *et al.*, 2015). The H2A.Z containing nucleosomes occurs in the transcription start and termination sites of ubiquitously transcribed genes and cover large parts of stress and developmentally regulated genes (Coleman-Derr and Zilberman, 2012). H2A.Z also marks other functional domains, e.g. potential sites of meiotic recombination (Zilberman *et al.*, 2008; Choi *et al.*, 2013; Yelagandula *et al.*, 2014). H2A.X is an evolutionary conserved variant scattered throughout the genome and upon phosphorylation of the serine 139 (γ -H2A.X) labels the sites of DNA damage repair (Friesner *et al.*, 2005; Lorković *et al.*, 2017). The recently discovered plant-specific variant H2A.W occurs in repetitive DNA regions, where it represses transposons and marks the sites of DNA damage repair (Yelagandula *et al.*, 2014; Lorković *et al.*, 2017). The H3 proteins include H3.1, H3.3 and CenH3 (CENP-A), representing the transcriptionally active, inactive and the kinetochore binding regions, respectively (Lermontova *et al.*, 2011; Stroud *et al.*, 2012; Wollmann *et al.*, 2012; Maheshwari *et al.*, 2015). CenH3 receives great attention owing to the fact that its mutations lead to production of haploids, a trait that could be used in the process of double haploid production (Ravi and Chan, 2010; Sanei *et al.*, 2011; Yuan *et al.*, 2014; Karimi-Ashtiyani *et al.*, 2015).

Unstructured histone N-termini (tails) are the rich substrate for post-translational modifications (PTMs) by methylation, acetylation and phosphorylation among others. Acetylation is associated with active chromatin, while methylation can have both permissive and repressive functions depending on the residue and the number of methyl groups in plants.

The most common plant genome DNA modification is cytosine methylation (5-methyl-2'-deoxy-cytosine or DNA methylation), where CG, CHG and CHH (H = A, T or C) represent the three functional DNA methylation contexts (Law and Jacobsen, 2010). DNA methylation can be established *de novo* at any cytosine by the RNA-directed DNA methylation (RdDM) pathway guided to the target sequences by small interfering RNAs with the perfect sequence homology (reviewed in e. g. Matzke and Mosher, 2014). Once established, DNA methylation is maintained by the activity of replication-coupled DNA methyltransferases specialized for each cytosine context, and by the corrective activity of RdDM (Du *et al.*, 2012; Zemach *et al.*, 2013; Baubec *et al.*, 2014). So far little is known about the significance and the functions of adenine methylation in plants (Vanyushin *et al.*, 1988; Fu *et al.*, 2015).

Nucleosomal DNA arrays are folded at multiple levels into higher order structures and eventually into the chromosomes (reviewed in e.g. Dixon *et al.*, 2016). Microscopic observations of variable chromatin staining intensity led to the early description of the darker chromosome stain called heterochromatin and the lighter chromosome stain called euchromatin (Heitz, 1928). Molecular experiments revealed that heterochromatin is normally repeat-rich/gene-poor, densely packed, and transcriptionally silent, while euchromatin is open, repeat-poor/gene-rich and transcriptionally active (Roudier *et al.*, 2011; Sequeira-Mendes *et al.*, 2014). Organisation and dynamics of the large chromatin domains and their functional significance in plants seems to be strongly influenced by the nuclear genome size and amount of repetitive DNA, but it is still not well understood. The small genome of *Arabidopsis* is organised as mostly randomly positioned chromosome territories with nuclear envelope (NE)-associated heterochromatic chromocentres (CCs) and nucleolus associated nucleolar organizer regions (NORs) (Fransz *et al.*, 2002; Pecinka *et al.*, 2004). In contrast, large genomes of e.g. cereals show Rabl-organisation with centromeres and telomeres clustered at the opposite nuclei poles. These patterns have recently been explored in detail by the chromatin conformation capture techniques (reviewed in Doğan and Liu, 2018). Currently, it remains unknown how representative such organisations are for different tissues, under changing environmental conditions and for species with intermediate DNA content. In addition, Hi-C experiments suggest that a combination of different factors, such as genomic composition, epigenetic modification, and transcriptional activity are involved in shaping global and local chromatin packing in *Arabidopsis* and rice (Grob *et al.*, 2014; Dong *et al.*, 2018). Hi-C applications to other crops will improve our knowledge on the role of chromosomes packing in the nucleus in modifying gene expression under stress conditions.

Chromatin organisation in somatic cell nuclei under ambient and stress conditions

Plants rapidly change gene expression during stress, to make a rational use of the existing resources and to minimize damage. Chromatin changes have been found practically after all types of applied abiotic and biotic stresses, and there is growing evidence that some epigenetic changes play important role in the fine tuning of stress responses (Kim *et al.*, 2010; Ding and Wang, 2015) (Fig. 1).

Nuclei of germinating *Arabidopsis* seeds appear mostly euchromatic, and heterochromatin is established only in response to the light stimulus (Mathieu *et al.*, 2003). Light-induced heterochromatin re-organisation leads to transcriptional reprogramming and activation of photosynthesis during germination (Bourbousse *et al.*, 2015). Light quality-induced phytochrome signaling may also cause repositioning of specific chromatin regions, e.g. chlorophyll A/B binding (CAB) locus in *Arabidopsis*, and thus influence gene expression (Feng *et al.*, 2014). Composition and intensity of solar radiation varies strongly depending on the season, geographical location or surrounding vegetation.

Ultraviolet A and B (UV-A/B, 280-400 nm) is the most energetic component of solar radiation, which damages membranes, proteins and DNA, and its intensity increases with

altitude and proximity to equator. Plants probably adapt to UV radiation as indicated by the constitutive expression of chromatin-remodeling factors and reduced sensitivity to UV damage, as was found in maize landraces at the tropical high altitude (Casati *et al.*, 2006, 2008). Interestingly, methyl cytosines have higher propensity to be involved in UV-induced pyrimidine dimers than normal cytosines, and their less efficient repair in heterochromatin leads to conversions into thymines (Willing *et al.*, 2016). Hence, UV radiation has a profound effect on both epigenome and genome stability.

Temperature fluctuations are common and involve rapid adjustment of cellular metabolism, growth and differentiation (Kotak *et al.*, 2007). Heat stress reduces chromatin compaction and coordinated organ specific transcriptional response via changes in nucleosome and H2A.Z occupancy (Kumar and Wigge, 2010; Pecinka *et al.*, 2010; Boden *et al.*, 2013; Lämke and Bäurle, 2017). Severe heat stress modulates chromatin structure, by increasing histone acetylation and decreasing H3K9me2 and eventually induces programmed cell death (Wang *et al.*, 2015b). Surprisingly, cold stress also leads to general chromatin de-condensation, as suggested by Hi-C analysis in rice, but specific regions may be subject to chromatin condensation and gene silencing (Liu *et al.*, 2017). Taken together, the data suggest that in a range of optimal temperatures, which are species-specific, chromatin is normally condensed, and de-condenses at suboptimal conditions. However, this hypothesis needs to be tested on a broader range of species and temperatures.

Vernalization is well-known example of cold induced chromatin change, i.e. acquisition of competence to flower only in response to a period of cold. In Arabidopsis, vernalization occurs via H3K27 tri-methylation and silencing of MADS box transcription repressor *FLOWERING LOCUS C (FLC)* (Rosa and Shaw, 2013; Whittaker and Dean, 2017). However, vernalization evolved multiple times in plants and its mechanism differs between species (Reeves *et al.*, 2012; Périlleux *et al.*, 2013; Ruelens *et al.*, 2013; Porto *et al.*, 2015). *VERNALIZATION 1 (VRN1)* is the major vernalization gene in cereals, which loses H3K27me3 and gains H3K4me3 during cold period (Oliver *et al.*, 2009; Diallo *et al.*, 2012). Temperature changes also lead to selective and transient activation of repetitive sequences (Steward *et al.*, 2002; Pecinka *et al.*, 2010; Tittel-Elmer *et al.*, 2010; Ito *et al.*, 2011). Recent studies suggested that this is due to the presence of the canonical cis-regulatory elements in the LTRs of specific stress-responsive transposon families (Cavrak *et al.*, 2014; Pietzenuk *et al.*, 2016). This could represent an evolutionary mechanism of dispersal for cis-regulatory elements in the genome and foundation of novel gene expression patterns (Ito *et al.*, 2011).

Reduced water availability negatively influences yield and resistance to other stresses. Effect of water stress on plant chromatin is not well understood, but data suggest that the responses are species-specific. Drought caused DNA methylation changes in the shoot apical meristems (SAM) of hybrid poplars (Gourcilleau *et al.*, 2010), and there were additional changes in DNA methylation and expression of phytohormone metabolism genes after re-watering (Gourcilleau *et al.*, 2010). In tomato, drought induced DNA methylation changes in

ABSCISIC ACID STRESS AND RIPENING 1 and *2* (*ASR1* and *ASR2*) genes (González *et al.*, 2011, 2013) and thus probably modified the ripening process.

In contrast, no consistent water stress-induced DNA methylation changes were observed in Arabidopsis and maize (Eichten and Springer, 2015; Ganguly *et al.*, 2017). Instead, H3K4me3 may represent a drought stress “memory” mark, which influences the transcriptional response during recurring stress in Arabidopsis (Ding *et al.*, 2012). The topic of chromatin mediated “epigenetic memory” has been recently reviewed in several papers (for example in Jablonka and Raz, 2009; Avramova, 2015; Lämke and Bäurle, 2017), and therefore we do not review it here.

Attacks of crops by pathogens may have severe consequences on plant vitality and yield, and can even cause lethality. Biotic stress defense mechanisms are fast evolving to match the evolutionary innovations on the pathogen side, which leads to a constant race between the host and the pathogen. Following infection by biotrophic or necrotrophic pathogens, plants typically reprogram gene expression from growth to defense (Moore *et al.*, 2011), which involves activation of the salicylic acid (SA) and the jasmonic acid/ethylene (JA/ET) pathways, respectively (reviewed in e.g. Glazebrook, 2005; Vlot *et al.*, 2009). Some pathogens developed strategies to directly affect chromatin modifiers. For example, the necrotrophic fungus *Alternaria brassicola* produces a toxin that inhibits Histone deacetylase (HDA) activity during infection (Matsumoto *et al.*, 1992; Kwon *et al.*, 2003). In line with this, knock-down of Arabidopsis HDA19 led to increased susceptibility to *A. brassicola*, while its overexpression activated JA/ET-regulated genes and triggered pathogen resistance (Zhou *et al.*, 2005). HDA19 represses SA biosynthesis and defense responses in Arabidopsis by suppressing transcription of *PATHOGENESIS RELATED (PR)* *PR1* and *PR5* genes (Tian *et al.*, 2005), indicating its negative role in SA-mediated defense responses (Choi *et al.*, 2012). Upon infection by Pst DC3000, *SIRTUIN2 (SRT2)*, another HDA involved in immune responses, is down-regulated, leading to higher SA production and expression of downstream defense genes (Wang *et al.*, 2010). In contrast, some HDAs regulate innate immunity positively (Latrasse *et al.*, 2017a). Although it is clear that histone acetylation (and de-acetylation) plays an important role in the regulation of defense-related genes, it is still not clear how HAT and HDAs are targeted to the target loci to allow genome-wide changes in gene expression (Ramirez-Prado *et al.*, 2018).

The effects of viruses on plant chromatin remain only poorly understood. In a pioneer study, Arabidopsis mutants deficient in DNA methylation and RdDM were found to be susceptible to geminiviruses (Raja *et al.*, 2008). The geminivirus genome consists of two single stranded DNA molecules, which replicate using the host’s replication machinery. The replicated virus dsDNAs are packed with nucleosomes and form tiny chromosome-like structures. The hosts’ defense responses involve suppression of gene expression by methylating the viral genome. Involvement of RNA PolIII and RDR6 (Jackel *et al.*, 2016),

indicates that the silencing is triggered by the non-canonical RdDM (reviewed in e.g. Matzke and Mosher, 2014).

In summary, this chapter shows that responses of chromatin to various stresses are diverse and in some cases highly adaptive. In many cases, we have only basic description of the stress-induced chromatin changes, and we still miss information on the persistence of these changes after recovery from the stress and about their heritability through mitosis and meiosis. Therefore, we expect that many future studies will focus on the identification of underlying mechanisms. In addition, it is expected that more groups of chromatin modifiers such as histone (de)methyltransferases and (de)ubiquitinylases will be firmly connected with stress-induced chromatin responses (Dhawan *et al.*, 2009; Wang *et al.*, 2015a; Dutta *et al.*, 2017). Understanding the involvement of chromatin in adjusting plant adaptation to diverse environmental challenges is of interest to a broad audience of plant scientists, considering that stresses are generally predicted to become exacerbated due to climate change and that they can strongly affect crop yields.

Chromatin organisation during mitotic and meiotic cell divisions

Chromatin undergoes drastic changes affecting its degree of compaction during the cell cycle. At the onset of cell divisions, the nuclear envelope (NE) disassembles allowing the access of cytoplasmic proteins to the nucleoplasm, including proteins which contribute to further chromatin condensation and spindle formation. Chromatin condensation is critical for the individualisation of chromosomes in order to guarantee proper distribution of genetic information between daughter cells. After segregation, chromatin is decondensed to restore its interphase state. To achieve this process, specific PTMs in histones occur, including the marker of condensed chromatin histone H3S10p (p = phosphorylation) and mitosis-specific PTMs such as histone H3T3p and H3T11p (Houben *et al.*, 2002; Zhang *et al.*, 2005). In maize, histone H3S28p and H3S50p delineate the pericentromeric and centromere regions during chromosome segregation, respectively (Zhang *et al.*, 2005). In the same species, changes in the level of histone H3S10p regulate sister chromatid cohesion (Kaszas and Cande, 2000), and an increase of H3 phosphorylation is linked to reduced acetylation levels at lysine 9 residues in histones H3 (Edmondson *et al.*, 2002). In barley, histone H4 acetylation (K5, K8, K12 and K16) is an important modification for chromatin structure, with H4K8Ac having no impact on chromatin structure from mitotic prophase to telophase (similar to H4K16Ac), while H4K5Ac and H4K12Ac, are more dynamic (Wako *et al.*, 2003, 2005). A survey of 17 plants species revealed distribution of histone H4K5ac differs between small and large genome species (Feitoza *et al.*, 2017). In most small genomes species ($2C < 5$ pg), H4K5ac was enriched in late condensing terminal regions but depleted in early condensing regions, while in large genome species, acetylation was more evenly displayed across the chromosome which were also uniformly condensed during the prophase stage.

The condensin complex is another main player in chromosome organization (Hirano *et al.*, 1997), which is probably recruited by H3S10p (Schmiesing *et al.*, 2000). Its basic structure

is given by the heterodimer of Structural Maintenance of Chromosomes (SMC) proteins SMC2 and SMC4, to which condensin I and II specific regulatory subunits associate. Condensin II accesses the cell nucleus before mitosis and its reduction partially reduces early H3 phosphorylation (Ono *et al.*, 2004). Subsequently, condensin I contributes to prophase chromatin compaction.

Similarly, the cohesin complex also contains two SMC subunits (SMC1 and SMC3), that are connected by an α -kleisin subunit (represented by one of the four homologues SYN1–4 in Arabidopsis), which recruits the HEAT repeat containing subunit SCC3. In addition, different proteins regulate cohesion establishment and maintenance (Bolaños-Villegas *et al.*, 2017). Cohesion is established at the onset of S phase and persists until the metaphase-anaphase transition and it is essential to resist the force of the spindle microtubules while chromosomes are aligned at the equatorial plate, allowing their accurate segregation to opposite poles (Fig. 2). At the beginning of anaphase, cohesion is released from chromosomes in two steps (Nasmyth, 2001). During prophase and prometaphase, cohesin is removed from chromosome arms. In the second step, before the onset of anaphase, remaining cohesin is released from centromeres allowing separation of sister chromatids. The PRECOCCIOUS DISSOCIATION OF SISTERS 5 – WING APART LIKE (PDS5-WAPL) complex eliminates cohesion from chromosome arms, whereas EXTRA SPINDLE POLE BODIES 1 (ESP1) separase removes centromeric cohesin via an ubiquitin-dependent cleavage of the α -kleisin in Arabidopsis (Liu and Makaroff, 2006; Pradillo *et al.*, 2015; De *et al.*, 2016). ESP1 is also important for the proper establishment of the radial microtubule network and nuclear/cytoplasmic domains (Yang *et al.*, 2009). Several studies have demonstrated that cohesin plays additional roles in DNA double-strand break repair (DSBR) and regulation of gene expression (Yuan *et al.*, 2011; Mehta *et al.*, 2012).

There are remarkable differences in chromatin condensation and organisation between mitosis and meiosis (Fig. 2). Meiotic chromosome condensation proceeds simultaneously to alignment of homologous chromosomes, programmed DSB formation, repair through homologous recombination (HR), and establishment and dissolution of the synaptonemal complex (SC). These processes are associated with striking morphological changes including dynamic variations in histone PTMs (Nasuda *et al.*, 2005; Oliver *et al.*, 2013). In leptotema, sites of DSB formation and their repair become marked with the γ -H2A.X (Shroff *et al.*, 2004). In pachynema, γ -H2A.X is completely lost from fully synapsed chromosomes. In barley, the first γ -H2A.X foci appeared only four hours after DNA replication in pollen mother cells (PMCs) (Higgins *et al.*, 2012; He *et al.*, 2017). In Arabidopsis, DSB hotspots are also associated with the markers of active chromatin, including histone H2A.Z variant and H3K4me3 modification, low nucleosome density and low DNA methylation (Choi *et al.*, 2013). Similarly, crossovers (COs) reside in genomic regions of “open chromatin”, which were identified based on hypersensitivity to DNase I digestion and H3K4me3 enriched nucleosomes in potato (Marand *et al.*, 2017). This is also likely the case for barley as DSBs and H3K4me3 are strongly localized towards the telomeres, whereas they are quite low in pericentromeric

regions (Baker *et al.*, 2015). However, only 20% of the DSBs are effectively associated with H3K4me3, leaving the other 80% unexplained in maize (Sidhu *et al.*, 2015; He *et al.*, 2017).

SWITCH1 (SWI1) is a plant-specific protein that regulates the switch from mitosis to meiosis (Mercier *et al.*, 2001; Agashe *et al.*, 2002; Sheehan and Pawlowski, 2009). Recently, it has been reported that SWI1 antagonizes WAPL during prophase I through a Sororin-like strategy in mitosis (Yang *et al.*, 2019). *swi1* mutants have altered distribution of acetylated histone H3 and dimethylated histone H3 (H3K4me2) (Boateng *et al.*, 2008). Interestingly, H3K4me2 is recognised by MALE MEIOCYTE DEATH 1 (MDD1), a PHD finger protein which acts as a transcriptional regulator, essential for Arabidopsis male meiosis (Andreuzza *et al.*, 2015). Arabidopsis plants defective for ARABIDOPSIS SKP1-LIKE1 (ASK1), a component of the SKP1-CUL1-F-box (SCF) ubiquitin ligase, also displays variations in acetylated histone H3 and H3K9me2 distribution patterns during meiosis (Yang *et al.*, 2006). The influence of these PTMs in meiotic HR has been highlighted in a recent work in which the disruption of H3K9me2 and DNA methylation pathways produce the epigenetic activation of meiotic recombination near centromeres (Underwood *et al.*, 2018; Choi *et al.*, 2018). These are regions normally suppressed for COs in order to avoid aneuploidies in the offspring (Rockmill *et al.*, 2006). In rice, the chromosomes are reprogrammed during the transition to meiosis under the control of the Argonaute protein MEIOSIS ARRESTED AT LEPTOTENE 1 (MEL1), increasing H3K9me2 and decreasing H3K9ac and H3S10p in order to promote synapsis and HR (Liu and Nonomura, 2016).

Entangling of meiotic prophase I chromosomes results in interlocks (Gelei, 1921), which could compromise chromatin integrity and result in chromosome mis-segregation. Here, the organisation and movements of chromosome termini (typically traced by labeling of telomeric repeats) and TOPOISOMERASE II (TOPII) activity are essential for removal of the interlocks (Martinez-Garcia *et al.*, 2018). At the onset of meiosis, telomeres attach to the NE and cluster forming a characteristic bouquet arrangement (Bass *et al.*, 2000). The mechanism of bouquet formation is not well understood and although it is widely conserved among eukaryotes, a characteristic bouquet arrangement is apparently not formed in Arabidopsis (Armstrong *et al.*, 2001). In Arabidopsis, telomeres present a complex behavior and are associated with the nucleolus throughout meiotic interphase and early prophase I. Clustering of telomeres around nucleolus allows pairing at the same time when axial elements of the SC are assembled (Roberts *et al.*, 2009). However, in other species, the subtelomeric regions undergo differential behaviour during premeiotic G2 and prophase I (Colas *et al.*, 2008; Richards *et al.*, 2012). In the large genome of cereals, the telomere bouquet precedes chromosomes synapsis (Phillips *et al.*, 2012; Barakate *et al.*, 2014), and although it is not required for pairing of homologous chromosomes, it may facilitate this process (Golubovskaya *et al.*, 2002). In this context, HR and synapsis start in the distal regions of the chromosomes in barley, but it has been suggested that this is likely related to the heterochromatin/euchromatin replication program rather than the telomere movements (Higgins *et al.*, 2012).

SMC complexes are essential during meiosis. Both condensin I and II complexes are important for maintaining the structure of meiotic chromosomes. Condensin I ensures normal condensation in centromeric and 45S rDNA regions, whereas condensin II eliminates interchromosome connections (Smith *et al.*, 2014). In addition, the cohesin complex is indispensable for proper pairing and HR (Golubovskaya *et al.*, 2006). Several meiosis-specific cohesin proteins have been identified in plants (Bolaños-Villegas *et al.*, 2017), but it is unknown how the replacement of the respective mitotic proteins takes place. ABSENCE OF FIRST MEIOTIC DIVISION 1 (AFD1), the meiosis-specific maize kleisin protein, is required for elongation of axial elements of the synaptonemal complex and also for normal bouquet formation (Golubovskaya *et al.*, 2006). In rice, if centromere cohesion is compromised, chromatids separate prematurely at anaphase I and chromosomes are intertwined, leading to chromosome bridges and fragmentation (Shao *et al.*, 2011). Mutants deficient for Arabidopsis SYNAPTIC 1 (SYN1), a meiosis-specific α -kleisin, present defects in arm cohesion during prophase I and problems in centromere cohesion from anaphase I onwards (Bai *et al.*, 1999; Cai *et al.*, 2003). In order to protect premature SYN1 depletion and thus cohesion at centromeres, SYN1 needs to be dephosphorylated by the protein phosphatases PP2AB' α and PP2AB' β (Yuan *et al.*, 2018). Precocious separation of sister chromatids at centromeres is also avoided by SHUGOSHIN-LIKE 1 and 2 (SGOL1 and SGOL2), and PATRONUS 1 (PANS1) (Cromer *et al.*, 2013; Zamariola *et al.*, 2014). This function is most likely conserved in both mitosis and meiosis as shown in rice (Wang *et al.*, 2011). In Arabidopsis, absence of functional ESTABLISHMENT OF COHESION 1/CHROMOSOME TRANSMISSION FIDELITY 7 (ECO1/CTF7), involved in the establishment of chromatid cohesion, also produces severe reduction of cohesion during meiosis (Bolaños-Villegas *et al.*, 2013). Furthermore, mutations in the two Arabidopsis WAPL genes, with a significant role in the removal of cohesin, lead to alterations in the organisation of heterochromatin and delayed cohesin removal during prophase I (De *et al.*, 2014). Concerning the SMC5/6 complex, the SUMO (Small Ubiquitin-like Modifier) E3 ligase activity conferred by METHYL METHANE SULFONATE SENSITIVITY 21 (MMS21) and NSE4A kleisin are required for normal meiotic progression and gametophyte development in Arabidopsis (Liu *et al.*, 2014; Diaz *et al.*, 2019; Zolkowski *et al.*, 2019).

Most of the information on the behavior of chromatin in meiosis derives from studies with fixed cells. However, innovative methodologies are being developed to enable the dynamic analysis of meiotic processes in live meiocytes. In a pioneer study, prophase I has been analyzed within PMCs of intact anthers in maize (Sheehan and Pawlowski, 2009) and recently live microscopy of male meiosis was performed at high resolution in Arabidopsis (Prusicki *et al.*, 2019). Such technology advancements will allow an in-depth analysis of dynamics of meiotic processes. Finally, the link between chromatin conformation and gene regulation during meiosis is still very obscure despite the number of genomic and transcriptomic studies in various plant species (Zhou and Pawlowski, 2014). However, most of these analyses have mainly been done with tissue covering the overall meiosis rather than specific meiotic stages, which is necessary to understand the gene expression pattern. In

addition, transcriptomic studies would also benefit from complementary proteomic experiments to address the regulation of gene/protein meiotic networks.

Chromatin dynamics during reproductive development

In Angiosperms, sexual reproduction starts with the development of flowers, when the SAM is transformed into the inflorescence meristem (IM) continuously producing the floral meristems (FM). Remarkably, the FM switches from an indeterminate fate to a determinate fate to give rise to all the organs of the flower, the gametes and the fruit. All reproductive development transitions are controlled by endogenous, hormonal or external environmental signaling pathways, which require complex gene regulatory networks involving transcription factors and epigenetic mechanisms.

The floral initiation is precisely coordinated via a complex gene network that integrates the age, photoperiod, temperature and hormonal signals (Andres and Coupland, 2012). At favorable conditions, the Arabidopsis systemic floral activator *FLOWERING LOCUS T* (*FT*, the florigen) or its orthologues in other species (e.g. *VRN3* in cereals) change SAM to IM. In Arabidopsis, *FT* expression is subjected to photoperiod and ambient temperature and is under a complex balance of active and repressive chromatin modifications involving both Polycomb Repressive Complex (PRC) 1 and 2 (He, 2012). Expression of *FT* target and flowering-pathway integrator, *SUPPRESSION OF OVEREXPRESSION OF CONSTANS 1* (*SOC1*) turns on the FM identity genes *APETALA 1* (*AP1*) and *LEAFY*, which promote the formation of the floral primordium (reviewed in Guo et al., 2015). The homeodomain transcription factor *WUSCHEL* (*WUS*) plays a central role in the process of FM determinacy by specifying the maintenance of stem cell activity within the organizing center of SAM, IM and FM (Cao et al., 2015). In cooperation with *LEAFY*, *WUS* activates the MADS-box transcription factor *AGAMOUS* (*AG*), which initiates the reproductive organ development. Thereafter, *AG* represses *WUS* activity to ensure the FM termination, and to promote all the finely tuned developmental transitions required for the proper development of floral organs. The repression of *WUS* is a perfect example to illustrate the importance of epigenetic regulatory mechanisms during FM termination. First, *AG* binds to the *WUS* locus, which allows the recruitment of the PRC2 catalytic subunit *CURLY LEAF* to mediate the deposition of H3K27me3 repressive marks on *WUS*. Then components of PRC1 complex recognize the H3K27me3, which results in the compaction of chromatin and further *WUS* repression. Thereafter, *AG* turns on the C2H2 zinc-finger transcription factor *KNUCKLES* gene (*KNU*), which terminates the inflorescence by stabilizing *WUS* repression (Bollier et al., 2018).

After meiosis (see the previous chapter), the male haploid gametophyte (microspore) undergoes an asymmetric division to produce a generative cell (GC) and a vegetative cell (VC), and the GC divides once more to produce two sperm cells (SCs) representing the male gametes (reviewed by e.g. Berger and Twell, 2011). SCs and VCs have very different chromatin characteristics, which determine also their fate, genome integrity and capacity to divide (Slotkin et al., 2009; Calarco et al., 2012; Ibarra et al., 2012). The SC nuclei are very compact and strongly repress transposons by maintaining high levels of H3K9me2, CG and CHG

methylation (Schoft *et al.*, 2009; Calarco *et al.*, 2012; Ibarra *et al.*, 2012; Hsieh *et al.*, 2016), whereas CHH methylation is generally low, but shows complex dynamics with temporal increases (Walker *et al.*, 2018). In contrast, the VC nuclei are de-condensed, without CenH3, H3K9me2 and DECREASED IN DNA METHYLATION 1 (DDM1), but rich in 21-nt siRNAs, suggesting loss of competence to divide, strongly reduced maintenance methylation control and activation of the non-canonical RdDM pathway (Schoft *et al.*, 2009; Slotkin *et al.*, 2009; Creasey *et al.*, 2014). This leads to the decreased CG methylation and increased CHH methylation levels and transcriptional activation of TEs in VC (Mosher *et al.*, 2009; Slotkin *et al.*, 2009; Calarco *et al.*, 2012; Creasey *et al.*, 2014; Martínez *et al.*, 2016; Martinez *et al.*, 2018). Furthermore, VCs show enrichment in H3K27me3, indicating high PRC2 activity (Borg and Berger, 2015). Functional significance of such extensive epigenetic reprogramming is still debated, but the activation of TEs in VC may represent a non-autonomous silencing mechanism, which switches off any potentially active transposons in the germline and thus preserves the genome integrity of the next generation. However, to what extent is this typical for plants other than Arabidopsis remains unknown. For example, cereals lack specific epigenetic factors present in Arabidopsis such as DEMETER (DME) or CHROMOMETHYLASE 2 (CMT2), but have multiple copies of other factors including DNA METHYLTRANSFERASE 1 (MET1), CHROMOMETHYLASE 3 (CMT3), DDM1 or specific subunits of Pol IV and Pol V (Zemach *et al.*, 2010, 2013; Li *et al.*, 2014; Haag *et al.*, 2014; Shi *et al.*, 2015; Bewick and Schmitz, 2017). In addition, the same factors in cereals may have different effects on DNA methylation such as ZmDDM1 that is required for the formation of mCHH islands via the RdDM pathway (Long *et al.*, 2018; Fu *et al.*, 2018). All this indicates a diversification and/or specialization of functions and a more important role of the small RNAs in epigenetic programming of cereal pollen. In rice SCs, there is high expression from *OsDRM2* and new small RNA pathway involving a non-canonical ARGONAUTE (AGO) and DICER-LIKE (DCL3) proteins, suggesting high CHH methylation levels (Russell *et al.*, 2012; Anderson *et al.*, 2013). In addition, there seem to be a specific variant of Pol V largest subunit in grasses (Trujillo *et al.*, 2018) and future studies will reveal whether these factors act in a novel RdDM pathway. Long intergenic noncoding RNAs (lincRNAs), correlated with H3K27me3 have been identified in the rice male gametophyte (Zhang *et al.*, 2014; Johnson *et al.*, 2018). Given the high and medium numbers of copies of putative orthologs of H3K27 and H3K4 demethylases, respectively, indicates that rice SCs may require more extensive reprogramming of repressive marks (Anderson *et al.*, 2013).

The replacement of canonical histones by specific variants is also characteristic of epigenetic control at male gametogenesis. In Arabidopsis SCs, the histone H3 variant, MALE GAMETE-SPECIFIC HISTONE 3 (MGH3), is the most abundant (Okada *et al.*, 2005; Ingouff *et al.*, 2007; Ingouff and Berger, 2010). This variant has been correlated with the loss of H3K27me3 methylation, due to the composition of the adjacent amino acid residues (Borg and Berger, 2015). In rice, a specific combination of H2A, H2B and H3 histone proteins has also been identified in SCs (Russell *et al.*, 2012; Anderson *et al.*, 2013). Histone H3.709 and H2A.Z are the most remarkable. Histone H3.709, although probably an ortholog of MGH3, is quite divergent in the amino acid composition. Replacement of histones also occurs in the

Arabidopsis VC, since CenH3 is progressively lost in centromeric heterochromatin when it begins to de-condense, while there is a loss of H3K9me2 marks, indicating a state of terminal differentiation (Schoft *et al.*, 2009; Mérai *et al.*, 2014). However, CenH3 and H3K9me2 persist in VC of rye and barley (Houben *et al.*, 2011; Pandey *et al.*, 2013), probably reflecting a temporal shift between pollination and fertilization in these species (Borg and Berger, 2015). In maize, the haploid microspores carrying a knock-down mutation in *hda108* gene collapsed and failed to develop properly, indicating that histone acetylation/deacetylation affects microspore viability (Forestan *et al.*, 2018). In *Brassica rapa*, H3K4me3 and H3K27me3 deposition is necessary for the regulation of the pollen wall construction (Shen *et al.*, 2019).

Female gametophyte develops in ovule according to the Polygonum type in ~70% of flowering plants, including e.g. Arabidopsis, maize, rice, wheat and soybean. In megasporogenesis, the diploid megaspore mother cell undergoes meiosis resulting in four haploid megaspores. One megaspore develops into the female gametophyte, while the other die. The formation and differentiation of the different cell types in the reproductive lineage are characterized by global changes in chromatin organisation. Histone modifications were observed via cytogenetic and chromatin reporter studies in Arabidopsis megaspore and also in the surrounding nucellar cells in maize (Garcia-Aguilar *et al.*, 2010; She *et al.*, 2010). Genetic analyses have identified DNA methylation acting upon the megaspore fate establishment, and also action of small RNAs silencing transposable elements in the female gametes in Arabidopsis and maize (Garcia-Aguilar *et al.*, 2010; Olmedo-Monfil *et al.*, 2010). The multicellular embryo sac consists of the egg cell, the central cell, two synergid cells and three antipodal cells. The female gametes, exhibit chromatin dimorphism as they express different histone H3 proteins with the egg cell expressing only the H3.3 variant, whereas there are both H3.1 and H3.3 proteins in the central cell (Ingouff and Berger, 2010). Due to the technically limiting accessibility to the female gametophyte, gene level resolution of the chromatin perturbations has not been reported to date. The histone modifications observed, suggest a global epigenetic reprogramming phase during the female gametophyte development. The epigenetic dimorphism of the two female gametes at the DNA methylation level, with the global demethylation of the central cell versus the non-CG DNA methylation of the egg cell highlights the different roles, which these two cell types are going to play in seed development (Pillot *et al.*, 2010). For an extensive review on the dynamics of the chromatin landscape on the female gametophyte development follow Baroux & Autran, (2015).

In the zygote, the parentally derived histone H3 variants are replaced before the first division of the embryo to reflect the content found in sporophytic cells (Ingouff and Berger, 2010). Two maternal epigenetic pathways are acting in the early embryo to regulate the paternal transcripts, the RdDM pathway and the histone chaperone complex Chromatin assembly factor 1 (CAF1). These pathways do not regulate genomic imprinting (Autran *et al.*, 2011). The central cell will give rise (upon fusion with one sperm cell nucleus) to the endosperm. In endosperm, maternally expressed genes will be suppressed by PRC2 complex, including central cell lineage specific H3K27 methyltransferase FERTILIZATION INDEPENDENT SEED 1/MEDEA (FIS1/MEA), implicated in the regulation of type I MADS-box genes and transition

from syncytial to cellularized stage (Zhang *et al.*, 2018). It should be noted that endosperm development is sensitive to parental genome dosage and the majority of imprinted genes reported are expressed from the maternal genome in the endosperm (reviewed in e.g. Gehring and Satyaki, 2017). Endosperm chromatin is characterized by a looser structure, DNA hypomethylation and decreased levels of H3K9me₂, when compared to somatic tissues and embryo (Baroux *et al.*, 2007; Pillot *et al.*, 2010). In contrast to embryo development, extensive demethylation occurs during endosperm development and this dynamic process allows for imprinting variation observed in maize and Arabidopsis (Gehring *et al.*, 2009; Waters *et al.*, 2013; Pignatta *et al.*, 2018). In maize, HDA101, and members of different chromatin remodeling complexes affect endosperm transfer cells leading to alteration in the kernel size (Yang *et al.*, 2016). Kernels of *hda108 hda101* plants showed a strong defective phenotype with fully or partially empty pericarp. Starchy endosperm tissue failed to accumulate starch or developed only partially in defective kernels, while the embryo showed abnormalities that varied from the presence of an undifferentiated aborted embryo to a defective embryo blocked at the coleoptilar stage (Forestan *et al.*, 2018).

Seeds are embedded in fruits, many of which are important source of food to humans. The best understood development of fleshy fruits is tomato, which displays remarkable characteristics related to chromosome structure, chromatin organisation and dynamics (Bourdon *et al.*, 2012). A major developmental feature is the increase in nuclear DNA content due to endoreduplication leading to cell hypertrophy, thereby influencing fruit growth and size (Chevalier *et al.*, 2014). Whether chromatin modifications are associated with endoreduplication still remains largely unknown. However, it was shown in Arabidopsis that endoreduplicated nuclei have less condensed heterochromatin (Schubert *et al.*, 2006; Jegu *et al.*, 2013). In tomato, DNA methylation decreases in the highly endoreduplicated pericarp tissue and is significantly reduced at the onset of fruit maturation and during ripening (Teyssier *et al.*, 2008; Zhong *et al.*, 2013), possibly to control the gene expression according to a tissue-specific endoreduplication status. Ectopic overexpression of the DAMAGED DNA BINDING PROTEIN 1 (DDB1), member of the DDB1-CUL4-based E3 ubiquitin ligase complex, regulating many developmental processes via chromatin remodeling, decreased the size of flowers and fruits in tomato (Liu *et al.*, 2012) via up-regulation of two positive regulators of endoreduplication *SIWEE1* and *SICCS52A* (Azzi *et al.*, 2015). Currently, there is increasing evidence for the epigenetic control during fruit organogenesis and epigenome dynamics plays an important role during fruit maturation and ripening in tomato (reviewed in Giovannoni *et al.*, 2017).

Plant chromatin modifications for the purposes of plant breeding

Decades of breeding and selection have narrowed down the pool of genetic variability in many crops (Palmgren *et al.*, 2015). Crop breeding programs have classically relied on sequence-based genetic variability of either natural or induced origin. These efforts have allowed the generation of varieties with an increased and more stable yield, and relatively well adapted to biotic and abiotic stresses. However, the exploitation of genetic variability existing within gene

pools has been limited. Furthermore, not all the heritable phenotypic diversity can be explained by sequence variation and has been termed as the missing heritability (Maher, 2008; Gallusci *et al.*, 2017). Such variation could have epigenetic basis.

Applicability of chromatin modifications for the purpose of crop improvement (Fig. 3) depends on their stability and heritability as the two key features. Epigenetic modifications may be of interest for breeders only if their regulatory effects are maintained through mitosis and ideally through meiosis. Here, DNA methylation and specific histone PTMs are the prime candidates for crop improvement, as they were mitotically transmittable for at least limited time in several species (Hyun *et al.*, 2013; Gaydos *et al.*, 2014; Avramova, 2015; Jiang and Berger, 2017; Kawakatsu *et al.*, 2017). This raises the possibility of employing them as tools for breeding in clonally-propagated crops, e.g. many fruit trees. However, for seed-propagated crops, specific chromatin modifications need to pass the epigenetic resetting barriers during gametogenesis and seed development in order to pass to the next generation (Pecinka and Mittelsten Scheid, 2012; Grossniklaus *et al.*, 2013; Iwasaki and Paszkowski, 2014; Kawashima and Berger, 2014; Quadrana and Colot, 2016; Roessler *et al.*, 2018). Here, DNA methylation seems the best candidate due to its stability and because PTMs are lost due to gametogenesis specific removal and replacement of the parental nucleosomes (Ingouff *et al.*, 2010; Quadrana and Colot, 2016).

Plant developmental processes determine a great number of traits of agronomical interest that have been targeted for selection in crops. Some of them are epigenetically regulated, either by DNA methylation or histone PTMs such as leaf shape, flowering time and flower development, male fertility, oil yield, fruit ripening, grain size, plant stature, inflorescence structure, branching plant architecture, boll setting rate, abscission rate, photoperiod responses, etc. (Zhang, 2012; Ong-Abdullah *et al.*, 2015; Xianwei *et al.*, 2015; Bull *et al.*, 2017; Latrasse *et al.*, 2017b; van Esse *et al.*, 2017; Fan *et al.*, 2018; Song *et al.*, 2018). Expanding evidence also shows that epigenetic control has an important role in the fine-tuning of the responses to biotic and abiotic stress (Gourcilleau *et al.*, 2010; Kim *et al.*, 2010; González *et al.*, 2011, 2013; Ding and Wang, 2015). This raises the possibility to generate or select variability of epigenetic changes to assist plant breeding. Stably inherited epialleles have been characterized for genes controlling some developmental processes. Examples of such epialleles in crops include: tomato *CNR* locus controlling fruit ripening (Manning *et al.*, 2006), oil palm *MANTLED* that regulates oil yield (Ong-Abdullah *et al.*, 2015), cotton *CONSTANS-LIKE 2* that determines photoperiod sensibility (Song *et al.*, 2017), rice *FERTILIZATION INDEPENDENT ENDOSPERM 1 (FIE1)*, which regulates plant height and flower development (Zhang *et al.*, 2012), *RAV6* affecting leaf angle and grain size (Xianwei *et al.*, 2015) or *SEMI-ROLLED LEAF 1 (SRL1)*, which determines rice cell wall formation (Li *et al.*, 2017).

Thus, epigenetic modifications are a source of phenotypic diversity and it is desirable to identify and/or generate novel epialleles of interest for crop improvement (Fig. 3). One possible approach is to select epigenetic variants among the natural diversity by exploiting DNA methylation states in different germplasms (Takuno *et al.*, 2016). This type of analysis has revealed large amounts of epigenetic variability in ecotypes, cultivars, landraces and wild

relatives (Eichten *et al.*, 2013; Schmitz *et al.*, 2013b; Garg *et al.*, 2015; Venetsky *et al.*, 2015; Kumar *et al.*, 2017; Song *et al.*, 2017; Liu *et al.*, 2018; Shen *et al.*, 2018). However, it requires good reference genomes and can be more time-consuming and tedious than mining genetic polymorphisms. The easiest way to link DNA methylation polymorphisms with phenotypes is to simultaneously monitor gene expression (Eichten *et al.*, 2013; Song *et al.*, 2017). However, this may be challenging for genes with tissue specific transcription.

Epialleles can be also generated artificially. Untargeted approaches employ cell culture (Mittelsten Scheid *et al.*, 2003; Ong-Abdullah *et al.*, 2015; Li *et al.*, 2017; Coronel *et al.*, 2018), abiotic stresses (Verkest *et al.*, 2015), transposon mobilization (Thieme *et al.*, 2017), or treatment with specific epigenetic inhibitors (Marfil *et al.*, 2012; Baubec *et al.*, 2014; Pecinka and Liu, 2014; Xu *et al.*, 2016; Zhu *et al.*, 2018). In addition, this can be achieved by the generation of epigenetic recombinant inbred lines (epiRILs) from crosses between wild type and maintenance DNA methylation mutants. Although epiRILs are a well-established system in *Arabidopsis* (Dapp *et al.*, 2015; Zhang *et al.*, 2016; Lauss *et al.*, 2018; Zhang *et al.*, 2018a), their use in crops is still in its infancy and might be influenced by the reproductive modality (Schmitz *et al.*, 2013a) and availability of viable epiregulator mutants (Anderson *et al.*, 2018). However, the current trends are directed towards controlled induction of the chromatin states. The RNA interference (RNAi) allows directing DNA methylation to specific positions and thus silencing the target loci. In addition, there are first studies demonstrating that modified CRISPR system using Cas9 or related nucleases (such as Cfp1) offer wide possibilities to change chromatin at specific loci (Liu and Moschou, 2018; Xie *et al.*, 2018). In this approach, chromatin remodelers, DNA or histone (de)methylases, transcription factors or specific protein domains can be, directly or via a marker peptide-antibody based system, fused to the catalytically dead Cas9 (dCas9), which leads to the recruitment of dCas9 to the locus of interest and chromatin change (Liu and Moschou, 2018; Xie *et al.*, 2018; Gallego-Bartolomé *et al.*, 2018). We predict that the number of dCas9 induced modifications will grow rapidly in the model plants as well as in crops. This approach has a great potential to shed more light on how the chromatin states are established, maintained and erased in plants. In addition, this could improve agriculturally relevant developmental or stress resistance-related traits in crops; however, the legal restrictions will most likely remain the main hurdle towards practical use of such inventions world-wide.

Chromatin modifications have emerged as a complementary source of variability contributing to plant phenotypic plasticity (Fig. 3). It could also address new challenges in crop improvement, including adaptive responses to environmental stresses. Since the emergence and inheritance of epigenetic variation differs from the genetic variants, current methods of trait mapping miss substantial phenotype-determining variation and thus may have reduced efficacy. Therefore, the relative contribution of genetic versus epigenetic variation remains unknown (Pecinka *et al.*, 2013). However, plant breeding using chromatin traits can be assisted by newly developed tools including process-based models (Hu *et al.*, 2015; Gallusci *et al.*, 2017), or epigenome-wide association studies (EWAS) (Rakyan *et al.*, 2011).

Future perspectives in plant breeding strategies

Classical plant breeding harnesses the genetic variation that is generated by homologous recombination during meiosis. For example, in cereals, a high amount of 20-30% (according to some sources up to 50%) of genes rarely recombine (Sandhu and Gill, 2002; The International Barley Sequencing Consortium, 2012; Higgins et al., 2014; Mascher et al., 2017), limiting the genetic diversity available for plant breeders and breaking the desirable combination of alleles in elite cultivars (Mascher *et al.*, 2017; Appels *et al.*, 2018; Ramírez-González *et al.*, 2018). In this context, a better understanding about the influence of the epigenetic makeup on meiotic recombination would contribute to development of novel strategies to modify the recombination pattern and to generate new elite crop varieties (Fig. 3). The ever increasing knowledge drawn from epigenetics studies in model and crop plants paves the way to applied perspectives and foreseen plant breeding strategies. The exploitation of epigenetic diversity is the forthcoming challenge for next plant breeding strategies, since chromatin modifications are tightly intertwined with plant phenotypic plasticity (reviewed in Pecinka et al., 2013; Gallusci et al., 2017). To cope with the improvement of genetic diversity resulting from intense plant breeding programs, epigenetic diversity may thus provide this opportunity to select for new traits related to plant adaptation to environmental constraints, crop yield or quality of plant products, pending a better understanding of all the associated regulatory mechanisms.

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Figure legends

Fig. 1. Overview of stress-induced chromatin changes and their potential trajectories.

Environmentally-induced stresses lead to genome wide changes of transcript levels. These changes are accompanied by dynamic changes influencing chromatin compaction and also gene expression. Transcriptional and chromatin changes can be correlated or uncorrelated and the exact hierarchy of events determining these changes can vary accordingly to the plant species and type of stress. There are some evidences that both transcriptional and chromatin changes can persist after the removal of stress and can be mitotically inherited. In a transcriptional memory gene - high expression levels are persistent for a prolonged period of time even after the end of a stress cue. In case of recurring stress, the transcriptional response to a second stress cue is modified compared to the response the first exposure to the same stress. Many cases of memory also involve chromatin dynamics at key regulatory loci (epigenetic memory). Despite transcriptional and chromatin/epigenetic memory, resetting and recovery are likely the overriding strategies used by plants to maximize fitness in time and space.

Fig. 2. Overview of chromosome organisation during mitosis and meiosis.

At the onset of mitosis, chromatin condensation is necessary to disassemble the interphase chromatin in a process driven by specific post-translational modifications (PTMs) in H3 and condensin complexes. In addition, cohesin complex is essential for defining chromosome structure by providing a physical linkage between sister chromatids until their segregation at anaphase.

Throughout meiosis, condensin complexes I and II are required to maintain the structural integrity of chromosomes. During leptotema, the histone variant H2A.X is rapidly phosphorylated to γ -H2A.X at double-strand break (DSB) sites. The synaptonemal complex (SC) forms between paired chromosomes at zygonema, and full synapsis is reached at pachynema. TOPOISOMERASE II (TOPII) activity is essential for removal of the interlocks formed when homologous chromosomes trap other chromosomes in between them. During late prophase I (diplonema/diakinesis) the SC disappears and further condensing homologous chromosomes are held together by chiasmata. During anaphase I, loss of cohesion between the arms of sister chromatids allows the segregation of homologous chromosomes to the opposite poles. Centromeric cohesion is released at the onset of anaphase II and sister chromatids segregate to form a tetrad.

Fig. 3. Applications of epigenetic variation for the purposes of plant breeding.

Natural epigenetic variation is relatively little explored and known cases were often selected by the phenotype and only later described to have epigenetic basis. Presumably, genome-wide screening for natural epigenetic variation will allow less biased use of the naturally occurring germplasms in the future. In contrast, induced epigenetic variation is provoked by humans either in a targeted manner towards specific genomic locus or an untargeted manner

with subsequent identification and selection of the modified loci. Choice of the method(s) is guided by the purpose, the species and its available resources. Some of the artificially produced epialleles fall under the GMO regulations.

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Figure 1

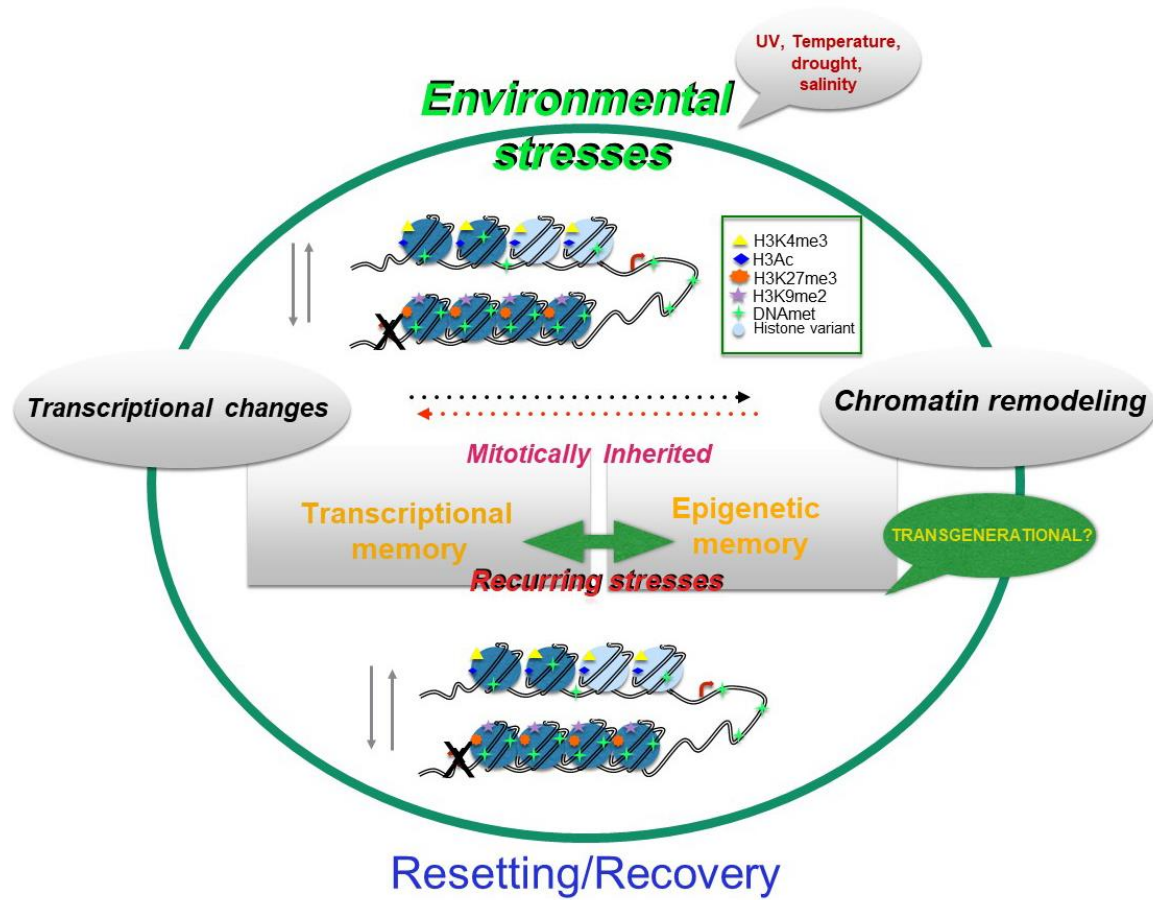


Figure 2

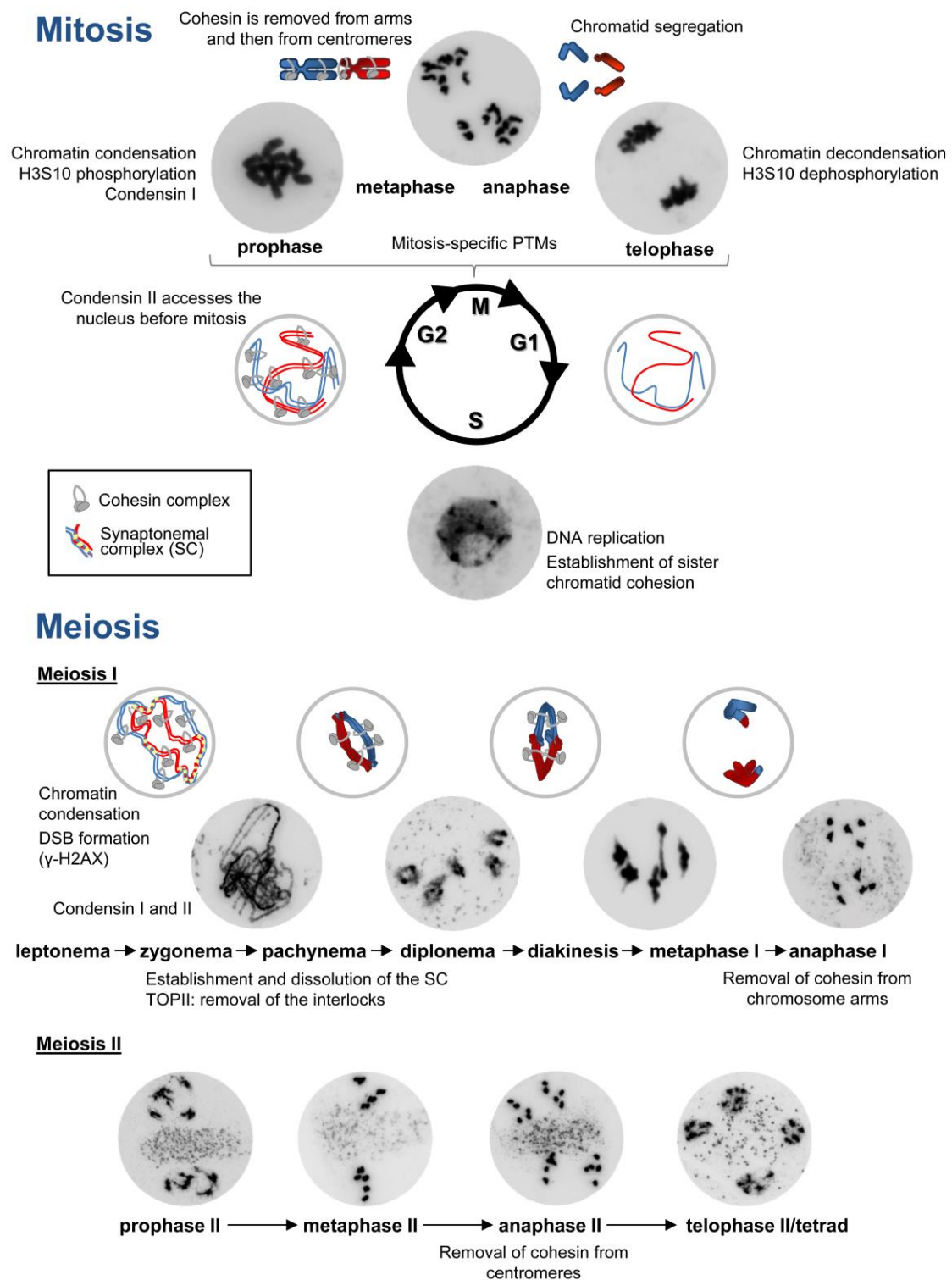


Figure 3

